#### (1) GENERAL INFORMATION:

- (i) APPLICANT: Parham, Christi L.

  Moore, Kevin W.

  Murgolo, Nicholas J.

  Bazan, J. Fernando
- (ii) TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: DNAX Research Institute
  - (B) STREET: 901 California Avenue
  - (C) CITY: Palo Alto
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US
  - (B) FILING DATE: 08-MAR-1999
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Ching, Edwin P.
  - (B) REGISTRATION NUMBER: 34,090
  - (C) REFERENCE/DOCKET NUMBER: DX0804K
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (650)852-9196
    - (B) TELEFAX: (650)496-1200
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1381 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:

15

| (B) L           | OCATION: 1321064  |     |
|-----------------|---|-----|
| (ix) FEATUR     | Æ:  |     |
|                 | IAME/KEY: misc_feature  |     |
| • •             | OCATION: 567  |     |
|                 | THER INFORMATION: /note= "nucleotides 567, 573, 1336, 69 designated C, but each may be A, C, G, or T" |     |
| (ix) ≒FEATUR    | Æ:  |     |
|                 | NAME/KEY: misc_feature  |     |
|                 | OCATION: 643  |     |
|                 | THER INFORMATION: /note= "nucleotides 643, 1287, and ed C, but each may be C or G"                    |     |
| (ix) FEATUR     | Æ:  |     |
| • •             | IAME/KEY: misc_feature  |     |
| * *             | OCATION: 772  |     |
|                 | OTHER INFORMATION: /note= "nucleotides 772, 806, and  |     |
| 1261 designat   | ed G, but each may be A or G"   |     |
| (ix) FEATUR     | RE:   |     |
| (A) N           | NAME/KEY: misc_feature  |     |
|                 | OCATION: 1236   |     |
|                 | THER INFORMATION: /note= "nucleotides 1236, 1260, 19 are designated T, but each may be G or T"        |     |
| (ix) FEATUR     | RE:   |     |
|                 | JAME/KEY: misc_feature  |     |
|                 | OCATION: 1247   |     |
|                 | OTHER INFORMATION: /note= "nucleotides 1247, 1257,  |     |
| 1293, and 130   | 2 designated C, but each may be C or T*   |     |
| (ix) FEATUR     | RE:   |     |
| (A) N           | NAME/KEY: misc_feature  |     |
|                 | OCATION: 1266   |     |
|                 | OTHER INFORMATION: /note= "nucleotides 1266 and 1298  |     |
| designated T,   | but each may be A or T*   |     |
| (xi) SEQUEN     | ICE DESCRIPTION: SEQ ID NO:1:   |     |
| TCGACCCACG CGTC | CGCGCT GCGACTCAGA CCTCAGCTCC AACATATGCA TTCTGAAGAA  | 60  |
| AGATGGCTGA GATG | GACAGA ATGCTTTATT TTGGAAAGAA ACAATGTTCT AGGTCAAACT  | 120 |
| GAGTCTACCA A AT | G CAG ACT TTC ACA ATG GTT CTA GAA GAA ATC TGG ACA   | 170 |
|                 | et Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr 1 5 10   |     |
| AGT CTT TTC ATG | TGG TTT TTC TAC GCA TTG ATT CCA TGT TTG CTC ACA   | 218 |

Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr

25

20

(A) NAME/KEY: CDS

|            |            |            | GCC<br>Ala        |            |            |            |            |            |            |            |            |            |            |            |            | 266 |
|------------|------------|------------|-------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
|            |            |            | AAG<br>Lys        |            |            |            |            |            |            |            |            |            |            |            |            | 314 |
|            |            |            | TAC<br>Tyr<br>65  |            |            |            |            |            |            |            |            |            |            |            |            | 362 |
|            |            |            | CAC<br>His        |            |            |            |            |            |            |            |            |            |            |            |            | 410 |
| Gly        | Pro<br>95  | Glu        | TGT<br>Cys        | Asp        | Val        | Thr<br>100 | Asp        | Asp        | Ile        | Thr        | Ala<br>105 | Thr        | Val        | Pro        | Tyr        | 458 |
|            |            |            | GTC<br>Val        |            |            |            |            |            |            |            |            |            |            |            |            | 506 |
| Ile        | Leu        | Lys        | CAT<br>His        | Pro        | Phe        | Asn        | Arg        | Asn        | Ser<br>135 | Thr        | Ile        | Leu        | Thr        | Arg<br>140 | Pro        | 554 |
|            |            |            | ATC<br>Ile<br>145 |            |            |            |            |            |            |            |            |            |            |            |            | 602 |
| Asp        | Leu        | Gly<br>160 | CCC<br>Pro        | Gln        | Phe        | Glu        | Phe<br>165 | Leu        | Val        | Ala        | Tyr        | Trp<br>170 | Thr        | Arg        | Glu        | 650 |
| Pro        | Gly<br>175 | Ala        | GAG<br>Glu        | Glu        | His        | Val<br>180 | Lys        | Met        | Val        | Arg        | Ser<br>185 | Gly        | Gly        | Ile        | Pro        | 698 |
| Val<br>190 | His        | Leu        | GAA<br>Glu        | Thr        | Met<br>195 | Glu        | Pro        | Gly        | Ala        | Ala<br>200 | Tyr        | Cys        | Val        | Lys        | Ala<br>205 | 746 |
| Gln        | Thr        | Phe        | GTG<br>Val        | Lys<br>210 | Ala        | Ile        | Gly        | Arg        | Tyr<br>215 | Ser        | Ala        | Phe        | Ser        | Gln<br>220 | Thr        | 794 |
| Glu        | Cys        | Val        | 225               | Val        | Gln        | Gly        | Glu        | Ala<br>230 | Ile        | Pro        | Leu        | Val        | Leu<br>235 | Ala        | Leu        | 842 |
|            |            |            | GTT<br>Val        |            |            |            |            |            |            |            |            |            |            |            |            | 890 |

| 240   | 245                      | 250                             |      |
|---|--------------------------|---------------------------------|------|
| GTC TGG AAA ATG GGC CGG<br>Val Trp Lys Met Gly Arg<br>255     |                          |                                 | 938  |
| GTC CTC CCA GAC ACC TTG<br>Val Leu Pro Asp Thr Leu<br>270 275 | Lys Ile Thr Asn Se       |                                 | 986  |
| AGC TGC AGA AGG GAG GAG<br>Ser Cys Arg Arg Glu Glu<br>290     |                          |                                 | 1034 |
| CCT GAG GAA CTC CTC AGG<br>Pro Glu Glu Leu Leu Arg<br>305     |                          | AGGTTTGCG GAAGGGCCCA            | 1084 |
| GGTGAAGCCG AGAACCTGGT C                                       | TGCATGACA TGGAAACC       | AT GAGGGGACAA GTTGTGTTTC        | 1144 |
| TGTTTTCCGC CACGGACAAG G                                       | GATGAGAGA AGTAGGAA       | GA GCCTGTTGTC TACAAGTCTA        | 1204 |
| GAAGCAACCA TCAGAGGCAG G                                       | GTGGTTTGT CTAACAGA       | AC AACTGACTGA GGCTATGGGG        | 1264 |
| GTTGTGACCT CTAGACTTTG G                                       | GCTTCCACT TGCTTGGC       | TG AGCAACCCTG GGAAAAGTGA        | 1324 |
| CTTCATCCCT TCGGTCCCAA G                                       | TTTTCTCAT CTGTAATG       | GG GGATCCCTAC AAAACTG           | 1381 |
| (B) TYPE:   |                          | ,                               |      |
| (ii) MOLECULE TYP   | E: protein               |                                 |      |
| (xi) SEQUENCE DES   | CRIPTION: SEQ ID N       | 0:2:                            |      |
| Met Gln Thr Phe Thr Met<br>1 5                                | Val Leu Glu Glu I<br>10  | le Trp Thr Ser Leu Phe<br>15    |      |
| Met Trp Phe Phe Tyr Ala<br>20                                 | Leu Ile Pro Cys L<br>25  | eu Leu Thr Asp Glu Val<br>30    |      |
| Ala Ile Leu Pro Ala Pro<br>35                                 | Gln Asn Leu Ser Vo<br>40 | al Leu Ser Thr Asn Met<br>45    |      |
| Lys His Leu Leu Met Trp<br>50                                 | Ser Pro Val Ile A<br>55  | la Pro Gly Glu Thr Val<br>60    |      |
| Tyr Tyr Ser Val Glu Tyr<br>65 70                              |                          | lu Ser Leu Tyr Thr Ser<br>75 80 |      |

His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu 85 90 95

Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
100 105 110

Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys 115 120 125

His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
130 135 140

Ile Pro Lys His Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly 145 150 155 160

Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Thr Arg Glu Pro Gly Ala 165 170 175

Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu 180 185 190

Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe 195 200 205

Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val 210 215 220

Glu Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe 225 230 235 240

Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys 245 250 255

Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Leu Pro 260 265 270

Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg 275 280 285

Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu 290 295 300

Leu Leu Arg Ala Trp Ile Ser 305 310

- (2) INFORMATION FOR SEQ ID NO:3:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1244 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..694

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 193
- (D) OTHER INFORMATION: /note= "nucleotide 193 designated C, may be C or T"  $\,$

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| C CGG GTC GAC CCA CGC GTC CGC CTG GTT TCC CCC TGG CTG ACA GTG Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val 1 5 10 15         | 46  |
|---|-----|
| CCT TGG TTC CTG TCC TGT TGG AAT GTT ACC ATT GGG CCT CCT GAG AGC Pro Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser 20 25 30    | 94  |
| ATC TGG GTG ACG CCG GGA GAA GCC TCC CTC ATC ATC AGG TTC TCC TCT Ile Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser 35 40 45    | 142 |
| CCC TTC GAC GTC CCT CCC AAC CTG GGC TAT TTC CAG TAC TAT GTC CAT Pro Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His 50 55 60    | 190 |
| TAC TGG GAA AAG GCG GGA ATC CAA AAG GTT AAA GGT CCT TTC AAG AGC Tyr Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser 65 70 75    | 238 |
| AAC TCC ATC GTG TTG GAT GGC TTG AGA CCC TTA AGA GAA TAC TGT TTA Asn Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu 80 85 90 95 | 286 |
| CAA GTG AAG GCG CAT CTC TTT CGC ACA TCC TGC AAC ACC TCT AGG CCC Gln Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro 100 105 110 | 334 |
| GGC CGC TTA AGC AAC ATA ACT TGC TAC GAA ACA ATG ATG GAT GCC ACT Gly Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr 115 120 125 | 382 |
| ACG AAG CTT CAA CAA GTC ATC CTC ATC GCC GTG GGA GTC TTT CTG TCG Thr Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser 130 135 140 | 430 |
| CTG GCG GCG CTG GCG GGC GGC TGT TTC TTC   | 478 |

|     | 145   |            |                   |       |       | 150   |       |       |       |       | 155  |       |       |       |                     |     |   |
|-----|-------|------------|-------------------|-------|-------|-------|-------|-------|-------|-------|------|-------|-------|-------|---------------------|-----|---|
|     |       |            | AAA<br>Lys        |       |       |       |       |       |       |       |      |       |       |       |                     | 52  | 6 |
|     |       |            | тат<br>Туг        |       |       |       |       |       |       |       |      |       |       |       |                     | 57  | 4 |
|     |       |            | ACG<br>Thr<br>195 |       |       |       |       |       |       |       |      |       |       |       |                     | 62  | 2 |
|     |       |            | CCA<br>Pro        |       |       |       |       |       |       |       |      |       |       |       |                     | 67  | 0 |
|     |       |            | TCT<br>Ser        |       |       |       |       | TAG   | CCTG! | rgg ( | GGTA | AGGG  | CT C  | TGAG( | CCGAG               | 72  | 4 |
| GAA | CTG   | CTG        | ATGT              | CCAT  | GT C  | AGCA  | CTTT  | A TGO | GAAT  | CCGG  | TCC  | rcca' | rrr ' | TCCT  | GTCCCC              | 78  | 4 |
| AAA | AGGC  | CCG        | TCAG              | rgcc' | rg Ty | GAAG  | ATGT  | A AC  | GGT   | CTCA  | TGG  | GGC   | GAC . | AAGC' | PTATTG              | 84  | 4 |
| ATT | rrrr. | CT         | TCAA              | ACTA  | AG AG | 3TTT  | rcta. | A TC  | ATAC  | GCGT  | TTT  | raga. | ATA . | ATTC' | TACAGA              | 90  | 4 |
| TAT | GTCC  | CCG        | AAAG              | ATTA  | AG A' | rttc' | rctt  | A AA  | CACT  | AAAA  | AGA  | CATG' | FAA ' | TTAT  | rtgtta <sub>.</sub> | 96  | 4 |
| GCA | AATG  | GGC        | GTCT              | GGCA  | CG C  | CTCT  | GACA  | C TT  | rttc  | GTCA  | GCA  | GCCA  | GGA ( | CACG  | AGGTCC              | 102 | 4 |
| CCT | CCTT  | GAT        | GAAG              | cccc' | TC G  | GGCA  | GACC  | A TG  | TCAC  | CTGT  | CCC  | AGCC' | TGC ( | CCCA  | AGAAGG              | 108 | 4 |
| GAC | ATTA  | AGT        | GGCC              | CTTC' | TT C  | TATA  | CCAA  | A CA  | CCTG  | GCTT  | GAA  | ATGTY | GAT ' | TAGC  | CCTGTA              | 114 | 4 |
| AAT | AGTT  | <b>ICA</b> | CAGA              | GATT. | AA G  | CCTT  | rrtt  | r cc  | CCCA  | AGTT  | AGG  | AATA  | AAA ( | GACT  | ТТААТТ              | 120 | 4 |
| AAC | rrrr  | ΓAA        | AAAA              | AAAA. | AA A  | AAAA  | AAAA. | A AA  | AAAA  | AAAA  |      |       |       |       |                     | 124 | 4 |

# (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 231 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro 1 5 10 15

Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile 20 25 30

Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro 35 40 45

Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Tyr 50 55 60

Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn 65 70 75 80

Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
85 90 95

Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
100 105 110

Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr 115 120 125

Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu 130 135 140

Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly 145 150 155 160

Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile 165 170 175,

Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp 180 185 190

Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val 195 200 205

Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr 210 215 220

Gln Asn Ser Gly Ala Val Cys 225 230

- (2) INFORMATION FOR SEQ ID NO:5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 337 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Arg Pro Thr Leu Leu Trp Ser Leu Leu Leu Leu Leu Gly Val Phe 1 5 10 15

Ala Ala Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala
20 25 30

Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser 35 40 45

Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg 50 55 60

Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met 65 70 75 80

Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe 85 90 95

Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr
100 105 110

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr 115 120 125

Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu 130 135 140

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser 145 150 155 160

Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr 165 170 175

Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe 180 185 190

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr 195 200 205

Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe 210 215 220

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp 225 230 235 240

Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe 245 250 255

Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys 260 265 270

Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro 275 280 285

Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu 290 295 300

Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val 305 310 315 320

Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr 325 330 335

Leu

- (2) INFORMATION FOR SEQ ID NO:6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 325 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: not relevant
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser 1 5 10 15

Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val 20 . 25 30

Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly 35 40 45

Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp 50 55 60

Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser 65 70 75 80

Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
100 105 110

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His 115 120 125

Gln Gly Pro Gln Ser

325

Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys 150 155 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg 185 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly 225 230 235 Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His 260 265 Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu 275 280 Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser 295 Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly 305 310